## CLAIMS

WHAT IS CLAIMED IS:

1. A method of characterizing a sample, comprising:

estimating a fluorescence impulse response ("*h(n)*") of the sample, based upon an expansion including Laguerre coefficients ("$\{c_j\}$"), the expansion being represented by the equation

$$h(n) = \sum_{j=0}^{L-1} c_j b_j^{\alpha}(n); \text{ and}$$

characterizing the sample by directly analyzing the Laguerre coefficients.

2. The method of claim 1, wherein the sample is selected from the group consisting of a biological tissue, a chemical, a biochemical sample and combinations thereof.

3. The method of claim 1, further including predicting the concentration of at least one biochemical component of the sample, wherein the sample is composed of a plurality of biochemical components.

4. A computer-readable medium having encoded thereon a computer-readable program code which when executed causes a computer to:

estimate a fluorescence impulse response ("*h(n)*") of a sample, based upon an expansion including Laguerre coefficients ("$\{c_j\}$"), the expansion being represented by the equation

$$h(n) = \sum_{j=0}^{L-1} c_j b_j^{\alpha}(n), \text{ and}$$

characterize the sample by directly analyzing the Laguerre coefficients.

5. An instrument for characterizing a sample, comprising

a computer-readable medium having encoded thereon a computer-readable program code which when executed causes the instrument to:

estimate a fluorescence impulse response ("*h(n)*") of a sample, based upon an expansion including Laguerre coefficients ("$\{c_j\}$"), the expansion being represented by the equation

$$h(n) = \sum_{j=0}^{L-1} c_j b_j^{\alpha}(n), \text{ and}$$

characterize the sample by directly analyzing the Laguerre coefficients.

6. The instrument of claim 5, wherein the instrument is selected from the group consisting of a spectrophotometer and a drug discovery analysis system.

7. A system comprising:

an excitation generator to excite a sample;

a fluorescence intensity measurement device to determine a measured fluorescence pulse trace;

a first interface to receive the measured fluorescence pulse trace; and

a processor to estimate a fluorescence impulse response ("*h(n)*") of the sample based upon the measured fluorescence pulse trace and an expansion including Laguerre coefficients ("$\{c_j\}$") and to characterize the sample by directly analyzing the Laguerre coefficients, wherein the expansion is represented by the equation

$$h(n) = \sum_{j=0}^{L-1} c_j b_j^{\alpha}(n).$$

8. The system of claim 7, wherein the sample is selected from the group consisting of a biological tissue, a chemical, a biochemical sample and combinations thereof.

9. The system of claim 7, further configured to analyze compositional changes in the sample.

10. The system of claim 7, further configured to analyze functional changes in the sample.

11. The system of claim 7, further configured to distinguish a tumor from normal tissue.

12. The system of claim 7, further configured to characterize a composition of an atherosclerotic plaque.

13. The system of claim 12, further configured to predict markers of atherosclerotic plaque vulnerability and rupture.

14. The system of claim 7, wherein the processor further predicts a concentration in the sample, the sample being a mixture of biochemical components.

15. The system of claim 7, further including an analytical instrument selected from the group consisting of a spectrophotometer, a cytometer and a drug discovery analysis system.

16. A method comprising:

obtaining an impulse response for a sample having been exposed to an excitation pulse;

deconvolving the excitation pulse from measured images;

estimating a first expansion coefficient ("$\{c_0\}$") of a plurality of expansion coefficients ("$\{c_j\}$") at each pixel of a plurality of pixels in an image and computing a map of the first expansion coefficient ("$\{c_0\}$");

generating a map of the higher expansion coefficients of the plurality of expansion coefficients ("$\{c_j\}$"); and

computing a map of lifetimes by constructing an impulse response function ("IRF") at every pixel for a predetermined number of time instances and interpolating a time point at which the IRF becomes 1/e of its maximum value, wherein the IRF is represented by the equation:

$$h(r,n) = \sum_{j=0}^{L-1} c_j(r) \cdot b_j^{\alpha}(n), n = 0,1,...,S-1.$$

17. The method of claim 16, wherein the sample is selected from the group consisting of a biological tissue, a chemical, a biochemical sample and combinations thereof.

18. The method of claim 16, further including detecting a physiological condition from the group consisting of a tumor and an atherosclerotic plaque.

19. The method of claim 16, further including predicting the distribution of concentration of at least one biochemical component of the sample images, wherein the sample is composed of a plurality of biochemical components.

20. The method of claim 16, further including monitoring an intracellular component and an activity of the intracellular component.

21. The method of claim 16, further including identifying a chemical with a biological activity for automated screening of the sample for new drugs discovery.

22. The system of claim 21, further configured to characterize drugs based on their chemical composition so high speed/throughput surveying and counting of the drugs is possible.

23. The system of claim 21, further configured to characterize a biochemical essay based on biochemical contents to facilitate high speed/throughput surveying/analysis of the essay.

24. The method of claim 16, further including sequencing a deoxyribonucleic acid (DNA) microarray.

25. A system comprising:

a fluorescence lifetime imaging device to generate a measured lifetime image for a sample;

a first interface to receive the measured lifetime image;

a processor to compute a lifetimes map for the sample by constructing a fluorescence impulse response ("*h(n)*") of the sample at every pixel, based upon an expansion including Laguerre coefficients ("$\{c_j\}$"), estimated in part based on the measured lifetime image, wherein the expansion is represented by the equation:

$$h(r,n) = \sum_{j=0}^{L-1} c_j(r) \cdot b_j^{\alpha}(n), n = 0,1,\ldots,S-1; \text{ and}$$

a second interface to transmit the lifetimes map.

26. The system of claim 25, wherein the sample is selected from the group consisting of a biological tissue, a chemical, a biochemical sample and combinations thereof.

27. The system of claim 25, further configured to analyze compositional changes in the sample.

28. The system of claim 25, further configured to analyze functional changes in the sample.

29. The system of claim 25, further configured to detect a physiological condition selected from the group consisting of a tumor and an atherosclerotic plaque.

30. The system of claim 25, wherein the processor further predicts a distribution of concentration in the sample images, wherein the sample is a mixture of biochemical components.

31. The system of claim 25, further configured to monitor intracellular components and activities.

32. The system of claim 25, further configured to identify a chemical with biological activity for automated screening of the sample for new drugs discovery.

33. The system of claim 25, further configured to perform microarray deoxyribonucleic acid (DNA) sequencing.

34. The system of claim 25, further including a fluorescence lifetime imaging microscopy (FLIM) microscopy system.

35. A computer-readable medium having encoded thereon a computer-readable program code which when executed causes a computer to:

obtain an impulse response for a sample having been exposed to an excitation pulse;

estimate a first expansion coefficient ("$\{c_0\}$") of a plurality of expansion coefficients ("$\{c_j\}$") at each pixel in an image and compute a map of the first expansion coefficient; and

generate a map of higher expansion coefficients of the plurality of expansion coefficients.

36. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to:

compute a map of lifetimes by constructing an impulse response function ("IRF") at every pixel for a predetermined number of time instances; and

interpolate a time point at which the IRF becomes 1/e of its maximum value, wherein the impulse response function is represented by the equation:

$$h(r,n)=\sum_{j=0}^{L-1} c_j(r)\cdot b_j^{\alpha}(n), n=0,1,...,S-1.$$

37. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to:

detect a physiological condition selected from the group consisting of a tumor and an atherosclerotic plaque.

38. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to analyze compositional changes in the sample.

39. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to analyze functional changes in the sample.

40. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to predicts a distribution of concentration in the image of the sample, wherein the sample is a mixture of biochemical components.

41. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to monitor an intracellular component and an activity of the intracellular component.

42. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to identify a chemical with a biological activity for automated screening of the sample to facilitate new drug discovery.

43. The computer-readable medium of claim 35, having encoded thereon a computer-readable program which when executed further causes a computer to perform microarray deoxyribonucleic acid (DNA) sequencing.

44. An instrument comprising:

a computer-readable medium having encoded thereon a computer-readable program code which when executed causes the instrument to:

obtain an impulse response for a sample having been exposed to an excitation pulse,

estimate a first expansion coefficient ("$\{c_0\}$") of a plurality of expansion coefficients ("$\{c_j\}$") at each pixel in an image and compute a map of the first expansion coefficient,

generate a map of higher expansion coefficients of the plurality of expansion coefficients,

compute a map of lifetimes by constructing an impulse response function ("IRF") at every pixel for a predetermined number of time instances, and

interpolate a time point at which the IRF becomes 1/e of its maximum value, wherein the impulse response function is represented by the equation:

$$h(r,n) = \sum_{j=0}^{L-1} c_j(r) \cdot b_j^a(n), n = 0,1,...,S-1.$$